

AC	AA053334;
XX	
DT	17-JUL-2001 (first entry)
DE	
XE	Human secreted protein-encoding gene 4 cDNA clone HWLFR02, SEQ ID NO:45.
XX	
KW	Human; secreted protein; proliferative disorder; cancer; tumour;
KW	fetal abnormality; developmental abnormality; haematopoietic disorder;
KW	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
KW	inflammation; allergy; neurological disorder; Alzheimer's disease;
KW	Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW	skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW	cardiovascular disorder; angiodenetic disorder; kidney disorder;
KW	gastrointestinal disorder; pregnancy-related disorder;
KW	endocrine disorder; infection; wound healing; vulnary;
KW	cell culture; chemotaxis; food additive; gene therapy;
KW	binding partner identification; chromosome 19; SS.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
CDS	166..1377
FT	*tag= a
FT	/product= "Human secreted protein"
FT	/transl_except= (pos:688..690, aa:Xaa)
FT	/transl_except= (pos:1123..1125, aa:Xaa)
FT	/transl_except= (pos:1156..1158, aa:Xaa)
FT	/transl_except= (pos:1267..1269, aa:Xaa)
FT	/note= "Xaa equals any of the twenty naturally occurring
FT	L-amino acids"
sig_peptide	166..246
FT	*tag= b
mat_peptide	247..1374
FT	*tag= c
FT	/product= "Mature human secreted protein"
XX	
PN	WO200134626-A1.
XX	
PD	17-MAY-2001.
XX	
PF	01-NOV-2000; 2000WO-US30045.
XX	
PR	05-NOV-1999; 99US-O163581.
PR	30-JUN-2000; 2000US-0215133.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Komatsoullis GA, Moore PA, Birse CE, Ni J;
XX	
DR	WPI; 2001-308778/32.
DR	P-PSDB; AAE01469.
XX	
PT	New nucleic acid molecules encoding 28 human secreted proteins for
PT	diagnosing, preventing, treating or ameliorating medical conditions and
PT	used as food additives or preservatives -
XX	
PS	Claim 1; Page 449; 562pp; English.
XX	
CC	AAD05300-AA05379 represent cDNAs corresponding to 28 human secreted
CC	protein genes, and AA051436-AAE01513 represent the proteins they encode
CC	AEE01514-AAE01544 represent human secreted protein fragments or variants
CC	The genes and their secreted proteins are useful for preventing,
CC	treating or ameliorating medical conditions, e.g., by protein or gene
CC	therapy. Pathological conditions can be diagnosed by determining the
CC	amount of the new protein in a sample or by determining the presence of
CC	mutations in the new genes. Specific uses are described for each of the
CC	28 genes, based on the tissues in which they are most highly expressed,
CC	and include developing products for the diagnosis or treatment of
CC	proliferative disorders, cancer, tumours, foetal and developmental
CC	abnormalities, haematopoietic disorders, diseases of the immune system,
CC	AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC	allergies, neurological disorders (e.g., Alzheimer's disease,
CC	Parkinson's disease), cognitive disorders, schizophrenia, asthma,

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 20:55:43 ; Search time 4666.15 Seconds
(without alignments)
6341.443 Million cell updates/sec

Title: US-09-970-076-1
Perfect score: 1414
Sequence: 1 agggaccgcggaggagggcc.....aaaaaaaaaaaaaaaaaaaaa 1414

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pi.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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1	1414	100.0	1414	9	AF421380	Homo sapi
2	1193.8	84.4	5540	9	AF279145	Homo sapi
3	1052.4	74.4	2112	9	BC012074	Homo sapi
4	890	62.9	1436	9	AK001463	Homo sapi
5	853.4	60.4	5220	10	AF378762	Mus muscu
6	542.8	38.4	4007	9	AK025429	Homo sapi
7	255.8	18.1	2126	9	AK057316	Homo sapi
8	236	16.7	1297	9	BC012475	Homo sapi
9	232.2	16.4	2026	9	AK055636	Homo sapi
10	207.8	14.7	1343	9	AY040326	Homo sapi
11	194.4	13.7	8107	2	AC025010	Homo sapi
12	194.4	13.7	8107	2	AC025010	Homo sapi
13	113	8.0	1189	9	AK002160	Homo sapi
14	92.8	6.6	2557	10	BC003908	Mus muscu
15	62	4.4	16248	30	AC053530	Homo sapi
16	61.2	4.3	1512	10	BC010278	Mus muscu
17	61	4.3	8712	6	AX344694	Sequence
18	60.2	4.3	52359	2	AC010772	Homo sapi
19	60	4.2	67676	2	AC102488	Mus muscu
20	59.4	4.2	6070	6	AX281468	Sequence
21	59.4	4.2	6070	6	AX346581	Sequence
22	59.4	4.2	6070	6	AX348804	Sequence
23	59.4	4.2	6668	6	AX346598	Sequence
24	59.4	4.2	13712	6	AX346433	Sequence
25	59.2	4.2	9219	6	AX251565	Sequence
26	59.2	4.2	9219	6	AX347328	Sequence
27	59	4.2	349980	6	AX344558	Sequence
28	58.4	4.1	74412	2	AC020767	Homo sapi
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30	58	4.1	6283	6	AX345737	Sequence
31	58	4.1	6283	6	AX348379	Sequence
32	58	4.1	6944	6	AX347467	Sequence
33	58	4.1	6944	6	AX349188	Sequence
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36	57.6	4.1	7076	6	AX347047	Sequence
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39	57.6	4.1	11015	6	AX356459	Sequence
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41	57.2	4.0	70816	2	AC101610	Mus muscu
42	57.2	4.0	349980	6	AX344556	Sequence
43	57	4.0	2379	3	DD31	X54452 D. discoideu
44	57	4.0	89128	2	AF001826	Homo sapi
45	57	4.0	126038	2	AC016068	Homo sapi

ALIGNMENTS

RESULT 1
AF421380

LOCUS AF421380 1414 bp mRNA linear PRI 13-NOV-2001
DEFINITION Homo sapiens anthrax toxin receptor mRNA, complete cds.

ACCESSION AF421380

VERSION AF421380.1 GI:16566412

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1414)

AUTHORS Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

TITLE Identification of the cellular receptor for anthrax toxin

JOURNAL Nature 414 (6860), 225-229 (2001)

MEDLINE 21557240

PUBMED 11700562

REMARK http://www.nature.com

REFERENCE 2 (bases 1 to 1414)

AUTHORS Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2001) Department of Oncology, University of Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA

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source		1..1414	
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Best Local Similarity 100.0%; Pred. No. 0;			
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DB	1	AGGACCGCGAGGAGGCGCGGATGGCGGTCCCTCAGGGTCTGCGGAGTTCGCGG	60
QY	61	agcgtgggaagagcagcctgctctcccggtgctggtggtggtggtggtggtggtggt	120
DB	61	AGCGTGGGAAGGAGCGGACCGCTCTCTCCCGGCTGCGGGCATGGCCACGCGGAGCG	120
QY	121	gagagcctcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt	180
DB	121	GAGAGCCTCGGCATCGGCTTCAGTGGCTCTCTTTGGCCACTCTGGTGTCTCATCTGCGC	180
QY	181	cgggcaaggggagcagcagggaggtgggtggtggtggtggtggtggtggtggtggtggt	240
DB	181	CGGCAAGGGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	240
QY	241	cttcattttgacaaatcagaaagtgtgctgacacactggaatgaaatctattacttgt	300
DB	241	CTTCATTTTGACAAATCAGGAAGTGTCTGCACCACCTGGAATGAAATCTATTACTTGT	300
QY	301	ggaacagtgtgctcacaaattcatcagccacagttgagaatgtcccttattgtttcttc	360
DB	301	GGAACAGTTGCTTCACAAATTCATCAGCCACAGTTGAGAATGTCCCTTTATTGTTTCTC	360
QY	361	caccgaggaacacaccttaatgaaactgacagagacagagacacacacacacacacacac	420
DB	361	CACCGGAGGAACACACTTAATGAAACTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	420
QY	421	agaagaacctcagaaagtctgcccagggagagacacttacatgcatgaaagttaagaag	480
DB	421	AGAAGAACTCCAGAAAGTCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	480
QY	481	ggccagtggcagagatttattatgaacacagacagaggggtacagagcagcagcgtcatcat	540
DB	481	GGCCAGTGAGCAGATTATTATGAAACAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	540
QY	541	tgtcttgactgagagagactcattgaagatctcttttcttattcagagagggaggtctaa	600
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QY	601	taggtctcagagactcttggtgcaattgtttactgtgtgtgtgtgtgtgtgtgtgtgtgt	660
DB	601	TAGGTCTCAGAGATCTTGGTGCATATTTTACTGTGTGTGTGTGTGTGTGTGTGTGTGT	660
QY	661	acagctggcccgaggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt	720

DB	661	ACAGCTGGCCCGGATGCGGACAGTAGGATCATGTGTTTCCCGTGAATGACGGCTTCA 720	
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DB	721	GGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCTGTCATCGAATTTCTAGCAGC 780	
QY	781	tgaacctccaccatattgtcagagagatcattcctcaagttgtgctgagagaaacgctt 840	
DB	781	TGAACCATCCACCATATGTGAGGAGAGTCAATTCAAGTTGTCTGTGAGAGGAACGGCTT 840	
QY	841	ccgacatgccgcaacgtggacaggttcctctcgagcttcaagatcaatgaatgactcggtcac 900	
DB	841	CCGACATGCCCGCAACGTGGACAGGGTCTCTGCAGCTTCAAGATCAATGACTCGGTAC 900	
QY	901	actcaatgagaagccctttttctgtggaagacacttatttactgtgtccagcgctatctt 960	
DB	901	ACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTACTGTGTCTCCAGCGCTATCTT 960	
QY	961	aaaagaagctggcatgaaagtgcactccaggtcagcatgacgatgagcggtcctctctttat 1020	
DB	961	AAAAGAAGTTGGCATGAAGCTGCACCTCCAGGTACGATGAACGATGCGCTCTCTTTTAT 1020	
QY	1021	ctceagttctgtcatcaccacacacactgttcttgcaggttccatctcctggtcgtcgtc 1080	
DB	1021	CTCCAGTTCTGTCTCATCATCACCACCACACACTGTTCTGACGGTTCATCTCGGCATCGC 1080	
QY	1081	cctgtgtacccctgttctcctgctcctgctcctcctcctcctcctcctcctcctcctc 1140	
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QY	1141	ctgcaactgtgattatcaagaggtccctccacccctcgcgagagagtgaggaataaa 1200	
DB	1141	CTGCACTGTGATTATCAAGAGGTCCCTCCACCCCTGCCGAGGAGTGAGGAAAAATAA 1200	
QY	1201	aataaatacaagaagaagaagaagaataccacagaaacagataaactaacacagc 1260	
DB	1201	AATAAATAACAAGAAGAAGAAGAATAATCCACAGAAACAGATAAAGCTAACACAGC 1260	
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DB	1261	CGTGCAACGTATTTATCAATGCTCTGAAATCATAGTCTCAATCTACACAGCTTTT 1320	
QY	1321	cctctagttccctgtattcaaatcccgagtgctcaaatcctcaataatagctatatgaat 1380	
DB	1321	CCTCTAGTTCCCTGTATTCAAAATCCAGGTCTTACATTCATTAATAATAGCTATATGAAT 1380	
QY	1381	caaaaaaataaaaaaataaaaaaataaaaaa 1414	
DB	1381	CAAAAAAATAAAAAAATAAAAAAATAAAAAA 1414	

RESULT 2
 AF279145 5540 bp mRNA linear PRI 09-MAY-2001
 LOCUS Homo sapiens tumor endothelial marker 8 precursor (TEM8) mRNA,
 DEFINITION complete cds.
 ACCESSION AF279145
 VERSION AF279145.2 GI:14017380
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 5540)
 AUTHORS St. Croix,B., Rago,C., Velculescu,V., Traverso,G., Romans,K.E.,
 Montgomery,E., Lal,A., Riggs,G.J., Lengauer,C., Vogelstein,B. and
 Kinzler,K.W.
 Genes expressed in human tumor endothelium
 JOURNAL Science 289 (5482), 1197-1202 (2000)
 MEDLINE 20407466
 PUBMED 10947988
 REFERENCE 2 (bases 1 to 5540)

AUTHORS St. Croix, B., Vogelstein, B. and Kinzler, K.W.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
 REFERENCE 3 (bases 1 to 5540)
 AUTHORS St. Croix, B., Vogelstein, B. and Kinzler, K.W.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-2001) Johns Hopkins Oncology Center, Johns Hopkins University, 1650 Orleans Street, Baltimore, MD 21231, USA
 REMARK Sequence update by submitter
 COMMENT On May 9, 2001 this sequence version replaced gi:9857405.
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 SEREARNRDLGAIYICGVKDFNETQLARIADSKDHVPVNDGFOALQGIHSLIKK
 SCIEILAAEPSTICAGESFOVVVNGRFRHARNVDRLVCSFKINDSVTLNRPFSVED
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 225..1835
 mat_peptide
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 /product="tumor endothelial marker 8"
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 Best Local Similarity 99.8%; Pred. No. 2.9e-306;
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 QY 61 agcgtggaagagcgagccctgtctcccggtgctgaggtgaggtgcgaggtgcgagcg 120
 DB 101 AGCGTGGGAAGGAGGAGGAGCCCTGCTCTCCCGGGTGGCGGATGCGGCGAGGCG 160
 QY 121 gagagccctcgagcgcggttcctcagtggtctcttggccactctggtgctcattcgcc 180
 DB 161 GAGAGCCCTCGCATCGCTTCCAGTGGCTCTTTTGGCCACTCTGGTCTCATCTGCGC 220
 QY 181 cgggcaaggggagcagggaggtgaggggttcagcctgctacggtgaggttcgagctgta 240
 DB 221 CGGGCAAGGGGAGCGAGGAGGAGTGGGGTCCAGCCTGCTACGCGGATTTGACCTGTA 280
 QY 241 ctctctttttgacaaatcagggaagtgtctgcacacacacacacacacacacacacac 300
 DB 281 CTTCTATTTTGGACAAATCAGGAAGTGTCTGCACACACACACACACACACACACAC 340
 QY 301 ggaacagttggctcacaaattcatcagccacagttgagagttgctttattgtttctc 360
 DB 341 GGAACAGTTCCTGCTACAAATTCACACACACACACACACACACACACACACACAC 380

361 caccggaggacaacaccttaataatgaaactgacagagacagagaacaaatccgtcaaggcct 420
 DB 401 CACCGGAGGAACAACCTTAAATGAACCTGACAGAAGACAGAGAACAATCCGTCAAGGCCT 460
 QY 421 agaagaactccagaagttctgcccagagagagacactacatgcatgaagatttgaag 480
 DB 461 AGAAGAACTCCAGAAGTTCTGCCAGGAGGAGACACTTACATGCTGAAGGATTGAAG 520
 QY 481 ggcagtgagcagatttattatgaaaaacagacagaggtacagagcagcagcgcacat 540
 DB 521 GGCAGTGAGCAGATTTATTATGAAACAGACAGAGGTACAGGACAGCCAGCGCTCAT 580
 QY 541 tgccttgactgagaggaactccatgaaatctctcttttttcttattcagagagggagctaa 600
 DB 581 TGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTCTATTTCAGAGAGGAGGCTAA 640
 QY 601 taggtctcgagatcttggtgtaattgtttactgtgtgtgtgtgtgtgtgtgtgtgtgt 660
 DB 641 TAGGTCTCGAGATCTTGTGTCATTTGTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 700
 QY 661 acagctggccgggattgaggacagtaaggtatgatttcccggtgtaagacagcgtttca 720
 DB 701 ACAGCTGGCCGGGATTGCGGACAGTAAGGATCATGTGTGTGTGTGTGTGTGTGTGTGT 760
 QY 721 ggcctgcaagggcatctccactcaattttgaaagaagctcctgcatgaaattcttagcgc 780
 DB 761 GGCCTGCAAGGCTCATCTCCACTCAATTTTGAAGAAGTCTCTGCTGCAAAATTTAGCAGC 820
 QY 781 tgaaccatccaccatgattgagcagagagtgatcttcaagttgtgctgagaggaacgcgtt 840
 DB 821 TGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTCTGAGAGGAACAGGCTT 880
 QY 841 cgacatgcccgaacgtggagacaggttcctctcagctcagctcaagaatcaatgactcggtcac 900
 DB 881 CGACATGCCCGCAACGTGGACAGGGTCTCTGCAGCTTCAAGATCAATGACTCGGTCTAC 940
 QY 901 actcaatgagaagcccttttctgtggaagacacttatttactgtgtccagcgcctatctt 960
 DB 941 ACTCAATGAGAGCCCTTTTCTGTGGAAGATACTTATTACTGTGTCCAGCGCTATCTT 1000
 QY 961 aaaaagttggcagaaagctgac 1020
 DB 1001 AAAAGAAGTTGGCATGAAAGCTGCACCTCCAGGTGACGATGACGATGGCCTCTCTTTAT 1060
 QY 1021 ctccagttctgcatcatcac 1080
 DB 1061 CTCCAGTTCTGTCTCATCATCACCACACACACTGTTCTGACGGTTCCATCTCGGCCATCGC 1120
 QY 1081 cctgctgactgcttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1140
 DB 1121 CCTGCTGATCTTGTCT 1180
 QY 1141 ctgactgtgattataaaggaggttcctcctcctcctcctcctcctcctcctcctcctcctc 1197
 DB 1181 CTGCACTGTGATTATCAAGGAGGTCTCTCCACCCCTCGCGAGGAGAGGTGAGGAAGA 1237

RESULT 3
 BC012074
 LOCUS
 DEFINITION Homo sapiens, Similar to tumor endothelial marker 8, clone
 MG:19967 IMAGE:4563020, mRNA, complete cds.
 ACCESSION BC012074
 VERSION BC012074.1 GI:15082332
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2112)
 AUTHORS Strausberg, R.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2002, 00:23:20 ; Search time 4666.15 Seconds
(without alignments)
4951.169 Million cell updates/sec

Title: US-09-970-076-1_COPY_104_1207
Perfect score: 1104
Sequence: 1 atggccacgcggagcggag.....gtgaggaataataaaaa 1104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_da.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_pl.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
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1	1104	100.0	1414	9	AF421380	Homo sapi
2	1090.8	98.8	5540	9	AF279145	Homo sapi
3	949.4	86.0	2112	9	BC012074	Homo sapi
4	853.4	77.3	5220	10	AF378762	Mus muscu
5	787	71.3	1436	9	AK001463	Homo sapi
6	542.8	49.2	4007	9	AK025429	Homo sapi
7	255.8	23.2	2126	9	AK057316	Homo sapi
8	236	21.4	1297	9	BC012475	Homo sapi
9	232.2	21.0	2026	9	AK055636	Homo sapi
10	207.8	18.8	1343	9	AY040326	Homo sapi
11	113	10.2	1189	9	AK002160	Homo sapi
12	92.8	8.4	2557	10	BC003908	Mus muscu
13	72.2	6.5	81017	2	AC025010	Homo sapi
14	48	4.3	1877	9	HS080080	Homo sapi
15	48	4.3	81017	2	AC025010	Homo sapi
16	47	4.3	7218	6	I66494	Sequence 14
17	44.4	4.0	229232	2	AC096624	Mus muscu
18	43.4	3.9	125020	9	AF429315	Homo sapi
19	43	3.9	174281	2	AC068338	Homo sapi
20	43	3.9	210651	2	AC105137	Homo sapi
21	41.4	3.8	7218	6	I66494	Sequence 14
22	41.2	3.7	146504	4	AC096884	Sus scrofa
23	40.6	3.7	1141	6	AX083744	Sequence
24	40	3.6	68639	9	AF443871	Homo sapi
25	40	3.6	158033	9	AC018926	Homo sapi
26	40	3.6	175264	9	AC011912	Homo sapi
27	40	3.6	235496	2	AC103312	Rattus no
28	39.6	3.6	140100	9	AC016778	Homo sapi
29	39.2	3.6	151559	2	AC015863	Homo sapi
30	39.2	3.6	170761	9	CNS05TER	Human chr
31	39.2	3.6	175826	2	AC109518	Homo sapi
32	39	3.5	60540	9	AL357059	Human DNA
33	38.8	3.5	195581	2	AC105611	Rattus no
34	38.8	3.5	197025	2	AC105642	Rattus no
35	38.6	3.5	166081	2	AL626786	Mus muscu
36	38.6	3.5	177531	9	AC005020	Homo sapi
37	38.4	3.5	163686	2	AC096159	Rattus no
38	38.4	3.5	195981	9	AC007652	Homo sapi
39	38.4	3.5	203200	9	AC008744	Homo sapi
40	38.4	3.5	219820	9	AC008738	Homo sapi
41	38	3.4	160496	9	AL450388	Human DNA
42	38	3.4	178295	2	AC021798	Homo sapi
43	38	3.4	181876	2	AC099065	Homo sapi
44	38	3.4	190562	2	AC096542	Homo sapi
45	38	3.4	216988	10	AC084217	Mus Muscu

ALIGNMENTS

RESULT	1	AF421380	1414 bp	mrna	linear	PRI 13-NOV-2001
LOCUS		Homo sapiens anthrax toxin receptor mRNA, complete cds.				
DEFINITION		AF421380				
ACCESSION		AF421380.1				
VERSION		GI:16566412				
KEYWORDS		human.				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1 (bases 1 to 1414)				
AUTHORS		Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.				
TITLE		Identification of the cellular receptor for anthrax toxin				
JOURNAL		Nature 414 (6860), 225-229 (2001)				
MEDLINE		21557240				
PUBMED		11700562				
REMARK		http://www.nature.com				
REFERENCE		2 (bases 1 to 1414)				
AUTHORS		Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.				
TITLE		Direct Submission				
JOURNAL		Submitted (19-SEP-2001) Department of Oncology, University of Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA				

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Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
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